

Leffers

## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTEC. / LOGY  
SYSTEMS  
BRANCH

RECEIVED

NOV 27 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/430,590B

Source:

1636

Date Processed by STIC:

11/13/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/430590B  
TECH CENTER 1000/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

G. Leffers

11/27/2000

1636

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000

TIME: 13:13:56

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: POULTER et al.  
4 POULTER et al.  
6 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS  
8 <130> FILE REFERENCE: 674521-2001.1  
10 <140> CURRENT APPLICATION NUMBER: 09/430,590B  
11 <141> CURRENT FILING DATE: 1999-10-29  
13 <160> NUMBER OF SEQ ID NOS: 79  
15 <170> SOFTWARE: PatentIn Ver. 2.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 1309  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Candida albicans  
22 <220> FEATURE:  
23 <221> NAME/KEY: variation  
24 <222> LOCATION: (1)..(1309)  
25 <223> OTHER INFORMATION: N stands for any nucleotide  
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30 ttgaagcaaa agaaaagtgt ggcacatcagc tagatatatta tatatgtata tgattagacc 180  
31 aacataaaac tagacgtcca aatatttatt tatttattta ttgatataata ttcttattta 240  
32 ttactgttat gatcttttga ttcacacaga gatttaatec aaatcaatac cttttgtttt 300  
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39 ttttttctct cttcttggtt cttagtattg gatttatagt tggtttatgc gacgtttgtg 720  
40 tcagggaaat aacaccttga tataagtcgt gcgtattagg tcaacatttg tgaataattt 780  
41 gcactcatcg agagccagga attagtataa aaagaagaga aaagaagat atttaggata 840  
42 tttattatat agggaccgag ttccaggaga cacttttagt gggcgtaaac ttcatcact 900  
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44 ttccgtgtat acaaacactt attgccaact tatggtgcgg aacttttatt gtctgaacca 1020  
45 aaatcaaaat cacatcattt aaatgaacgt tgacataaat agattcttta ttcaatagaa 1080  
46 acaatttctt cctttntctt ttctttgtat tantggttag atttccattc catatacaca 1140  
47 caagatgtca acgaaatcag caaatccaac tgctgtcaat tcatttaaty caaaccactc 1200  
48 caactatgac gtttttagac cttcattcac cccagttttg gtcaatatat tcttagtaca 1260  
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52 <210> SEQ ID NO: 2  
53 <211> LENGTH: 1340  
54 <212> TYPE: DNA  
55 <213> ORGANISM: Candida albicans  
57 <220> FEATURE:  
58 <221> NAME/KEY: variation  
59 <222> LOCATION: (1)..(1340)  
60 <223> OTHER INFORMATION: N stands for any nucleotide

P-6

OK

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000

TIME: 13:13:56

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

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W--> 65 atgatggctc aatgattnat tttagggttta tatgtggatg atattctaat ggacagaatc 180  
W--> 66 tcagatggaa tcgttatcag atttgttgaa caagagagag tttatttcgc gtnaaaatca 240  
67 atttaggtct catgacagaa tatgtgagat aaaaatgtcca cgtaagcaaa actgggtgat 300  
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73 aattaaaatt gtgttgtgaa atattctacat cctacaaaagt tcaagacatt tattgatggt 660  
74 atattcaaa gactcgatgt tgagaatgat aataacctga accaagacgc tacaatgct 720  
75 aattgagtaa ttcgtaattg ctaaacacacg ccatttcgaa tcaggggagt gttggtttat 780  
76 ggcagcttgg tgtcagggaa ataacacctt gatataagtc gtgcgtatta ggtcaacatt 840  
77 ggtgaaaaat ttgcactcat cgagagccag gaattagtat aaaaagaaga gaaaagaaag 900  
78 atatttagga tatattatat atagggaccg agtttcagga gacacttta gtgggcgtaa 960  
W--> 79 actncattac tntgtttttt gcttattgca aataatccct atcgtgtact aggactaatt 1020  
80 ctacagaata ttccgtgtat acaaacaaaa tcagacttct tggtaagccc agccgaaaca 1080  
81 gccatacttc tagtggatct ttctatacta caacattcac actgcttgac ctacaactac 1140  
82 acatacttct tgttataaag gcaatctatc acacaaaaga ttactgttg actcacaaga 1200  
83 tatcaactgt actaataaag gagtgcattc tatgaccttt ggagaggaac tatgtataat 1260  
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85 attagcaccg acacgacctg 1340

88 &lt;210&gt; SEQ ID NO: 3

89 &lt;211&gt; LENGTH: 556

90 &lt;212&gt; TYPE: DNA

91 &lt;213&gt; ORGANISM: Candida albicans

93 &lt;400&gt; SEQUENCE: 3

94 caacattggg tgaaaaaatt tgcactcatc gagagccagg aattagtata aaaagaggag 60  
95 aaagaaggta tttaggatat ttattatata gggaccgagt ttcaggagac acttttagtg 120  
96 ggcgtaaact tcattcactc tgttttttgc ttattacaaa ttatcaccta tcgtgtacta 180  
97 ggactaatte tcacgaatat tccgtgtata caaacattat acgtgtctgt aactacgoga 240  
98 aactacttcg totcagtttt ttgttacaaa caactttccg tatagacctg agattttgc 300  
99 agcttgattg aatggaagag tttactaaa gaccagaaa gtgttttata gataacatgt 360  
100 agatatataa aaatgttata ttacaaatga cttccaaaag aaactgtacg aattttgcgt 420  
101 tttattaaaa accagttcct gaaaactagt atcttagctt cagtacattt agcccaccta 480  
102 aattggacct atgacaagtt ctactttccc gacaatgcta atatagagca gttttcttct 540  
103 cttcttcttc ctcgtc 556

106 &lt;210&gt; SEQ ID NO: 4

107 &lt;211&gt; LENGTH: 2112

108 &lt;212&gt; TYPE: DNA

109 &lt;213&gt; ORGANISM: Candida albicans

111 &lt;400&gt; SEQUENCE: 4

112 atttaatatg ttggtattgg ctactgccaa cttcttagct gatgcagatg ccattgttaa 60  
113 tattgttaaa ttgggttaaat agtatgaagg aagcttttgc aggcgttggt atttttttca 120  
114 ccaattatta tcatcacctg cggagggttag tcaatttgag attgtgcgag ggaaaaaaa 180  
115 cgacctccat acactacctc aagtataagt ccagtcacat tgttcgctat agagagattt 240  
116 cctagccgga atgcacgaca atcctgagac ggaagtcgat cgtcgatgcc catggtgcgt 300

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000

TIME: 13:13:56

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

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119 aaatacaaaa tcaagatata attatatacc ttacttgtct atattgtttt ataatacatt 480
120 cttcagatat ttaaatttct gtgtatcacc ctataaaaca gagatacatt cagtgcattt 540
121 agtatactga gtgaactggg acctgtgaca ttcaagataa ctgtttcacg cagctgggca 600
122 gacgaacacc aatagtatga tgaagaactg acctgggtgt aagaggtttg atggagtttc 660
123 ttttttttag aagaggttga taagccaaca gatgaggaqt aacaagtaac tcgcaacatt 720
124 gtataacata agtttacatc aaatcagaat ttactaagaa aatcaatcca ttcaaaaggc 780
125 actcaatcat tgaaaaaaac agcttuatga gttagacggtc tgttcatatg aaacaattga 840
126 aaggggtgaa tattgtttgg aaaattatat aattcatgtc aaactgggag gcttaaatta 900
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168 tyttcgttgt cgtcattgtc gattagtttc agtttctaga ggtgaaattt tctatggcac 780

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## RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/09/430,590B

TIME: 13:13:56

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

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214 ccattcaact aacccaattg aattgaatga caatttgatc tccaaagagg gattcatttc 3540
215 tattctggag agataaacgt cattgtttag gaaagagcaa gagataagaa atccttttga 3600
216 tattgtatat atattattaa tgttatatta cactattgtt tgtttgtttg ttataattat 3660
217 atgtgagatt tcatatglaa gatgttgtta tctctttcca ttatttagct tttttgaaaa 3720
```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000

TIME: 13:13:56

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

218 agctatcaat ggcctccacgt tt 3742

221 <210> SEQ ID NO: 6

222 <211> LENGTH: 1438

223 <212> TYPE: DNA

224 <213> ORGANISM: Candida albicans

226 <220> FEATURE:

227 <221> NAME/KEY: variation

228 <222> LOCATION: (1)..(1438)

229 <223> OTHER INFORMATION: N stands for any nucleotide

231 <400> SEQUENCE: 6

232 gtgtagatgc aataggtgta tgaatgtat ctatgattata tcatgaagcc cttgcccaata 60

233 aaatctagcc aaaaatttgt gtactgcaat tgttcgctat agagagatat cctagccgga 120

234 atgcacgaca atcctgagac ggaagtcgat cgtcgatgcc catggtgcgt ggtgaaaaat 180

OK -> 235 tntcttagaa aatttgttct ttccctcaac tgcttttaag agaagggagg ttcaagtggg 240

236 ttaagtacga cggtcacaaa gattgcggct tatgagggcc gaactgagtt gaaatacaaa 300

237 atcaagatat aattatatac cttacttgtc tatattgttt tataatacat tcttcagata 360

238 tttaaatttc tgtgtatcat cctataaaac agagatacat tcatgacatt tagtatactg 420

239 agtgaactgg tacctgtgac attcaagata actgtttcgc gcacgctggc agacgaacag 480

240 caattctgta attgtcgtag agtagcaaca aatcttccc atgattggta cttgtgttaq 540

241 tctacacgac atgtgttttg gtacacttga actgtatgtc caagaatgga aacatatgcg 600

242 ggaaggacgc gaaagatgag tttggtagag aagggataag aactgtaaaa tatattatgt 660

243 agttatata ttaattatg ggaattgag tgtttatct gttcaacaag tttcaaccgt 720

244 agagattaca tttaaagtct gtggtcgaaa tccacaagat acagcaaat catgaattca 780

245 cctattttaa tcaagtttac caagcaccat tgcctagaac ttgccatate atcaattaaq 840

246 tcagacatta ctaatttgag caaagctttt agcttaattg gccaaactaat ttaagtogaa 900

247 ttggtaatgc aatctgttct tcatttgagt cgttgcctac ggtcccatga cacatccatt 960

248 tgattgtttt aattcagagc attatccacc ataactctca gtaatatcat taacagtttt 1020

249 acycttaata agcatagaaa gttgtatgaa gttgtctcct aggtatgcta gagagatttg 1080

250 tatatacgac cagtaaaagag gtgtagtagg tgtttactgt agggtaaat gcaattgact 1140

251 tgagttgata gcggttatta caaagtata gattcaacaa attaagacaa gtaccaaacy 1200

252 ataggccgaa tgtgacttat accgttgaag ttcaagcgtt tttacaaaat agaaatgtga 1260

253 gattaatgag ttcgacaaat gttttactag atactattaa ttccgatgta ctatataagt 1320

254 ttaaccagct ataaccggca gagcagactt cctgaaactc aaattgggtt tgtttggact 1380

255 tgagttacac cacaagtttt gacaatcgtg aggacatagc aacctatcaa gccactca 1438

258 <210> SEQ ID NO: 7

259 <211> LENGTH: 1304

260 <212> TYPE: DNA

261 <213> ORGANISM: Candida albicans

263 <400> SEQUENCE: 7

264 tgaagatctg gctttggcca aagtatcagc tgcattagat actgtcattg gcattggctt 60

265 gaaccactg gctgtggatg taactgtgga gccaaaagct cgtaaaagct tggcgttcat 120

266 ggagaaaaat cttttaacag acattgtata aacgttgaag attaaagaaa aaaaaaacag 180

267 aaagattacg aataatttgt ttttaattgg tgggtatgag gtgttgcgca gtcgactcaa 240

268 caattctctt ttggtgcaca aagttggttt tatggtcaac aattacggag tactgtctgt 300

269 agtgaagtgt aatctaagac ggaatgcct cctttacatt tgtttctatt ctcttaaaat 360

270 acatattcaa ttgtgtgttt taattgaaaa tttgttcate ttcactctgat gattgtgtaa 420

271 tctttgcggg gggggggcgt gtcatgaacc aatctctttg agtcatagga cgaatcatcc 480

272 tattgtgact catggctcat ctactctct tactaatctc ttacttcate tgtttactat 540

273 aaatatgtct actactctc tattttatta cctcgtttac tatttttatt caatatatga 600

09/43 90B 6

Partial listing  
of Sequence 16

<210> 16  
<211> 6140  
<212> DNA  
<213> Candida albicans

<400> 16  
agtaaaaaaa gaagaaaaaa aagctaaaaat tgggacaata tgctaagtat atatagggga 60  
agacgtcgaa cagcaaccac ggaaaaataa tagtgattgt ctttatccgt tattggctgg 120  
atggcgacgc cacaacctga aatttggttc caactgttga ggatgattta tgtttgtgat 180  
tagaactaaa atcattcgag aaaaaaggaa taggagagaa ccaactttag tctgtgtaaaa 240  
agtaacatct gccaatata aactatacgt agtccaaata atttacggta tatttctgta 300  
ccccctcttg gcaatatcac aagaatatca taatgttcat gaaccctctt tgaacacgta 360  
gacaagtaaa cccaatgagg gggcagtgtt ctattcttgt aaactgcgca ccaaaaacgg 420  
ggcttaaaaa ataagttatg aaaactataa ataaccatga aaatcaccct actcccttcc 480  
tcccttcctt ccttccttcc ttccttttct cttttcctct acccacacta ctcaaatgt 540  
tcggtatttt tgaggaaaac tacgattctg tttacaaagg caaccacgaa gccaaagttct 600  
ctcacgaagc agttgctggg gctgcttcat ttgctgctgt caagttgttt gaagatagac 660  
aaagaagaga agggaaacca gttagtcacg cctttgctaa agaagcttta gctgctattg 720  
ctggtggaga agtcgacaaa ttatttgaaa ccaaagggtt ggactatttg gatagagaga 780  
gacttagaga tcaagctatc aacaacgctc aaagagggtta cgacgacat tacggtcaac 840  
acgaagaatg gtctccagaa cacagaccac cttttgacta ccaaagatat taagtagaaa 900  
ctgtgtagtg aatttacaat ttttttgaca agaattaact taaacctcgt ttttaggttt 960  
tgtgcggtt ttgtcaattg acgatcctgt atatttcgtc ataattcaca cattcttaaa 1020  
attatgcaca catccttgaa atgtgttaat attccaaca ttatcaatta tatgtgttca 1080  
gaattgggtg caaagtattc aactcaattc acgctatata aaccttaca attctctaca 1140  
tttttatatt tttttatatt ggcttttctt ttagaatcaa tcaatacttt ttttatcatt 1200  
tagatacatc tttcatctat taatagatta tctttctata tatcaaaaaca cgacacagtc 1260  
acgtgccaaa aaggatataa gaaggaactt cagaaaatta attttctgat tatactactt 1320  
actagatttc ataaagtcaa tatctgattg atacaacttg gttcattatt cataaaactt 1380  
tacaactaat tdnacaagaa aacccnaca aaaaatcna atnaaataat cnnnnnaata 1440  
ttataattaa ttaattacaa aaaaaaaca aaaaatacac acacacatac acacacacaa 1500  
aatcttggtg caaaaaaaa aaaataataa taatataata agaattaatt aacaatgtcg 1560  
tttccacgga cacattcacc aagaccatct gggtcacgag aacaggaaga tctcactctg 1620  
atgattaaag ctttttagaga ttcaatggaa gctaagcttg acttgcatc gcagaagctt 1680  
actgctttgg tagcaaact tcccagaacg gacgaagggt ttgaagattt atcacaaagg 1740  
atcactgttc ttaaaaatca tcaaaaagca tttttgccca aacaagaaaa agaaatcgga 1800  
agtcttctcc acagacaaa agaggaagaa ggtgatatta aggatttcaa aacagtcgtt 1860  
ggtgaagaaa aagaagaatt gcaccaggtt gaagatttcg ttttaaaaaga tcaagaagaa 1920  
ttacgaacg tcgaaaagaa agttttgaaa gaagaagaag aattgcaaaa agtggaagag 1980  
tcaatggaaa aggaaaaaca agagttatac caggttgaag actttatttt gcaaaagat 2040  
gagacggtaa agaaacttg agaaagcaat caatctcaac aggaaccata tacacctgca 2100  
acttctggtt cggatcagag attcagatct caacaacctt acattggaaa taccttagcg 2160  
caggatctag cattaattcc aaaattagat ctggaaattt gcaaaattgc agtcaaatat 2220  
ccaaaattat ttgaaacaaa attaagacca ccaccacca gagactttca atataaaatt 2280  
caactcacag accacactca aatttattca aaaccatata aatgcaatca agaagaacaa 2340  
gctctcatca aggatttcat caatgaaaaa ttagaagcag gcgttttggg accagctcca 2400  
attgatgctt ggttacacct aatatttcca atcagaaaaa ccaatgccaa ccaatcctcc 2460  
accaaaatag cagttgattt aagacgtctc aataaggcca cagtacgaat gtacacttat 2520  
ccaacagaca caaagacct cttatcctca ctaacagatt cccactattt tagcgcttta 2580  
gacttaaaaga atgcgttcta tcaggtaagc atacacaagg atagtataaa atattttggg 2640  
atttcaacat ccgaggggaa ttattgcttt acaactttac cgtttgagc aatcaattcc 2700  
ccaaccatct ttactaactt tgtgagacag atttttagag ggatcccatg tatatttata 2760  
tacatggatg atatcctcat ccatactaaa accttacttg accacatgtc attactcagg 2820  
agaatcatgg agaaactaaa tgagcatcag tttcaaatga attataacaa gatgcaatta 2880  
ttaacaacaa aaatcaattt cttagggtac agcattcaag cgaacaaaat atcaccagat 2940  
atttccaaaa ttcaagcaat acaaaattgg gaattgccca cgaccactac tcaaatcaga 3000  
gcatttgta atttcagcaa ccactttcgc atcttcatcc cagaaatagc aaaatttact 3060

See  
item 10  
on Enon  
summary  
sheet

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

FYI



VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000  
TIME: 13:13:57

Input Set : A:\Poulter1.app  
Output Set: N:\CRF3\11132000\I430590B.raw

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:873 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16  
L:873 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16  
L:873 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16  
L:873 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:873 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
L:1367 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
L:1367 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
L:1381 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
M:340 Repeated in SeqNo=20  
L:1384 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
L:1385 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
L:1433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:1434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:1521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1634 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25  
L:1634 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25  
L:1634 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25  
L:1634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
L:1634 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25  
L:1635 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25  
L:1635 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000

TIME: 13:13:57

Input Set : A:\Poulter1.app

Output Set: N:\CRF3\11132000\I430590B.raw

L:1635 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25  
 L:1635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
 M:340 Repeated in SeqNo=25  
 L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1728 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27  
 L:1728 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27  
 L:1761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:2375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
 L:4009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72